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============================================================
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2010; month=2; day=2; hr=15; min=29; sec=59; ms=922; ]
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Application No: 10575374   Version No: 3.0

Input Set:

Output Set:

Started: 2010-01-20 15:19:46.905
Finished: 2010-01-20 15:19:49.644
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 739 ms
Total Warnings: 48
Total Errors: 1
No. of SeqIDs Defined: 68
Actual SeqID Count: 68

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
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W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)

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            Input Set:


           Output Set:



             Started:   2010-01-20 15:19:46.905
            Finished:   2010-01-20 15:19:49.644
             Elapsed:   0 hr(s) 0 min(s) 2 sec(s) 739 ms
      Total Warnings:   48
        Total Errors:   1
 No. of SeqIDs Defined:  68
   Actual SeqID Count:   68

Error code      Error Description

W   213         Artificial or Unknown found in <213>  in SEQ ID (38)
                This error has occured more than 20 times, will not be displayed
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gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta   180

aaagcatata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa   240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac   300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc   360

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attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt   480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga   540

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<213>   Saccharomyces cerevisiae

<300>
<308>   NCBI / NC_001136
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<400>   2

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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35   40   45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
    50   55   60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65   70   75   80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
            85   90   95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
            100   105   110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
        115   120   125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
    130   135   140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145   150   155   160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly
195 200 205

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
210 215 220

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<213> Saccharomyces cerevisiae

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<223> point mutation

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<211> 44
<212> PRT
<213> Saccharomyces cerevisiae

<400> 4

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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
        35   40

<210> 5
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<212> DNA
<213> Saccharomyces cerevisiae

<400> 5

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tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa   240

gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt   300

gattcagaag caggtgggac aggtgaactt ttggattgga actcgatttc tgactgggtt   360

ggaaggcaag agagccccga gagcttacat tttatgttag ctggtggact gacgccagaa   420

aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg   480

gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt cgtcaaaaaa tgctaagaaa   540

<210>   6
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<212>   PRT
<213>   Saccharomyces cerevisiae

<400>   6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val
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Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val
            20   25   30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr
        35   40   45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr
    50   55   60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys
65   70   75   80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe
                85   90   95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp
            100   105   110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp
    130   135   140

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
145   150   155   160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys
                    165   170   175

Asn Ala Lys Lys
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<212>   DNA
<213>   Saccharomyces cerevisiae

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<212>   PRT
<213>   Saccharomyces cerevisiae

<400>   8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35   40   45

Asp Pro Val Ile Ala
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<211>   516

<212> DNA
<213> Saccharomyces cerevisiae

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ggcattgata tcgtccaact gcacggagat gagtcgtggc aagaatacca agagttcctc   180

ggtttgccag ttattaaaag actcgtattt ccaaaagact gcaacatact actcagtgca   240

gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt   300

gaacttttgg attggaactc gatttctgac tgggttggaa ggcaagagag ccccgagagc   360

ttacatttta tgttagctgg tggactgacg ccagaaaatg ttggtgatgc gcttagatta   420

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aacaaaatag caaatttcgt caaaaatgct aagaaa   516

<210> 10
<211> 172
<212> PRT
<213> Saccharomyces cerevisiae

<400> 10

Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly
1   5   10   15

Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp
            20   25   30

Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His
        35   40   45

Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val
    50   55   60

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala
65   70   75   80

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala
                85   90   95

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val
                100   105   110

Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly
        115   120   125

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile
    130   135   140

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser
145   150   155   160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
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<211> 561
<212> DNA
<213> Saccharomyces cerevisiae

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aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa   240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac   300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc   360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt   420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg aactcgatt   480

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<210> 12
<211> 187
<212> PRT
<213> Saccharomyces cerevisiae

<400> 12

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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35   40   45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
        50   55   60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65   70   75   80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
                85   90   95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
                100   105   110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
        115   120   125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
        130   135   140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145   150   155   160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
                165   170   175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly
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<210>   13
<211>   111
<212>   DNA
<213>   Saccharomyces cerevisiae

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ggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a   111

<210>   14
<211>   37
<212>   PRT
<213>   Saccharomyces cerevisiae

<400> 14

Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly
1   5   10   15

Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val
            20   25   30

Lys Asn Ala Lys Lys
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<210> 15
<211> 612
<212> DNA
<213> Saccharomyces cerevisiae

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<221> mutation
<222> (22)..(22)
<223> point mutation

<220>
<221> deletion
<222> (612)..(612)
<223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAAAG
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<400> 15
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gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta   180

aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa   240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac   300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc   360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt   420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt   480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga   540

ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta   600

agcggaggtg tg   612

<210> 16
<211> 204
<212> PRT
<213> Saccharomyces cerevisiae

<400> 16

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
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Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
                20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
            35   40   45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
            50   55   60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65   70   75   80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
                85   90   95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
                100   105   110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
            115   120   125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
            130   135   140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145   150   155   160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
                165   170   175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
            180   185   190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
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<210> 17
<211> 36
<212> DNA
<213> Saccharomyces cerevisiae

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<221> mutation
<222> (1)..(1)
<223> missing sequence before base 1 of SEQ17, corresponding to base 63
        7 of wild-type: GAGACAAATGGTGTAAAAGACTCT

<400> 17
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<210> 18
<211> 12
<212> PRT
<213> Saccharomyces cerevisiae

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
1   5   10

<210> 19
<211> 43
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<213> Artificial Sequence

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<223> first of a pair of peptides (together with peptide C2), that asso
        ciate into an anti-parallel coiled coil (Biochemistry 37 (1998),
        12603-12610)

<400> 19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala
1   5   10   15

Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu
            20   25   30

Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly
        35   40

<210> 20
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
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        ociate into an anti-parallel coiled coil (Biochemistry 37 (1998),
         12603-12610)

<400> 20

Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu
1   5   10   15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys
            20   25   30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp